BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.1.2 [Nov-13-2000]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2

x_dropoff: 50   expect: 10.000   wordsize: 11   Filter ☑   **Align**

Sequence 1 lcl|seq_1 **Length** 137 (1 .. 137)

Sequence 2 lcl|seq_2 **Length** 612 (1 .. 612)
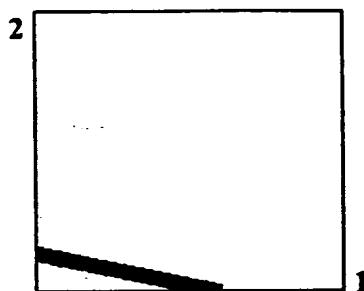
NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

```
Score =  148 bits (77), Expect = 5e-34
Identities = 81/83 (97%)
 Strand = Plus / Minus
```



```
Query: 1   ccggtaagtaaacagtcagaaaattagcatgaaagcagtttagcattgggaggaagcaca 60
           ||||||||||||||i|||||||||||||||||||||||||||||||||||||||||| ||
Sbjct: 85  ccggtaagtaaacagtcagaaaattagcatgaaagcagtttagcattgggaggaagctca 26


Query: 61  gatctctagagctgtcctgtcgc 83
           ||||||||||||||| ||||||
Sbjct: 25  gatctctagagctgtcttgtcgc 3
```

```
CPU time:     0.02 user secs.      0.06 sys. secs      0.08 total secs.

Gapped
Lambda    K        H
   1.33    0.621    1.12

Gapped
Lambda    K        H
   1.33    0.621    1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1
Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1
```

EXHIBIT B
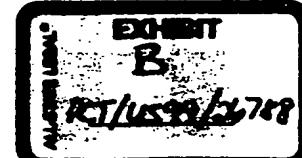
```
Number of sequen    better t    10.0: 1
length of query: 137
length of database: 2,635,864,967
effective HSP length: 22
effective length of query: 115
effective length of database: 2,635,864,945
effective search space: 303124468675
effective search space used: 303124468675
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 18 (35.3 bits)
```